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OM nucleic - nucleic search, using sw model

Run on: July 15, 2008, 17:58:23 ; Search time 15168 Seconds
(without alignments)
11333.508 Million cell updates/sec

Title: US-10-720-177-1
Perfect score: 2100
Sequence: 1 cacaaaatccggcggaatcca.....ttgggattaagtgcctgcag 2100

Scoring table: IDENTITY_NUC ←
Gapop 10.0 , Gapext 1.0 ←

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_in:*
13: gb_om:*
14: gb_ba:*
15: gb_htg1:*
16: gb_htg2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Match | Length | DB | ID | Description |
|--------|-----|-------|-------|--------|----|----------|-------------------|
| | 1 | 2100 | 100.0 | 2100 | 2 | CQ817719 | CQ817719 Sequence |

| | | | | | | |
|------|--------|-------|--------|----|--------------|--------------------|
| 2 | 2100 | 100.0 | 2100 | 2 | DD028154 | DD028154 Method fo |
| c 3 | 2004.4 | 95.4 | 110000 | 14 | BA000036_26 | Continuation (27 o |
| c 4 | 2004.4 | 95.4 | 349136 | 14 | BX927155 | BX927155 Corynebac |
| c 5 | 2004.4 | 95.4 | 349980 | 2 | AX127151 | AX127151 Sequence |
| c 6 | 1924.8 | 91.7 | 110000 | 14 | AP009044_26 | Continuation (27 o |
| 7 | 1588.2 | 75.6 | 1629 | 2 | BD164926 | BD164926 Novel pol |
| 8 | 1588.2 | 75.6 | 1629 | 2 | AX122809 | AX122809 Sequence |
| 9 | 1435.2 | 68.3 | 1468 | 2 | AX764345 | AX764345 Sequence |
| 10 | 1435.2 | 68.3 | 1468 | 2 | EA032755 | EA032755 Sequence |
| 11 | 845 | 40.2 | 861 | 2 | DD097361 | DD097361 CORYNEBAC |
| 12 | 845 | 40.2 | 861 | 2 | DD097362 | DD097362 CORYNEBAC |
| 13 | 845 | 40.2 | 861 | 2 | AX063819 | AX063819 Sequence |
| 14 | 845 | 40.2 | 861 | 2 | AX063821 | AX063821 Sequence |
| c 15 | 669.4 | 31.9 | 110000 | 14 | BA000035_25 | Continuation (26 o |
| c 16 | 415.6 | 19.8 | 453 | 2 | BD164925 | BD164925 Novel pol |
| c 17 | 415.6 | 19.8 | 453 | 2 | AX122808 | AX122808 Sequence |
| 18 | 365.4 | 17.4 | 1371 | 14 | DQ019448 | DQ019448 Micrococc |
| 19 | 365.4 | 17.4 | 1380 | 2 | E17152 | E17152 Micrococcus |
| 20 | 296.8 | 14.1 | 1395 | 4 | AY702086 | AY702086 Aspergill |
| 21 | 296.8 | 14.1 | 110000 | 4 | AP007175_15 | Continuation (16 o |
| c 22 | 279.2 | 13.3 | 110000 | 14 | CP000781_17 | Continuation (18 o |
| 23 | 275.6 | 13.1 | 110000 | 14 | CP000656_24 | Continuation (25 o |
| c 24 | 275 | 13.1 | 110000 | 14 | CP000431_73 | Continuation (74 o |
| c 25 | 273 | 13.0 | 110000 | 14 | BA000040_53 | Continuation (54 o |
| c 26 | 272.2 | 13.0 | 110000 | 14 | BA000040_43 | Continuation (44 o |
| c 27 | 258 | 12.3 | 110000 | 14 | CU234118_33 | Continuation (34 o |
| c 28 | 245.6 | 11.7 | 110000 | 14 | CP000454_44 | Continuation (45 o |
| 29 | 241 | 11.5 | 110000 | 14 | CP000781_13 | Continuation (14 o |
| c 30 | 240 | 11.4 | 110000 | 14 | CP000494_37 | Continuation (38 o |
| 31 | 231 | 11.0 | 110000 | 14 | CP000521_11 | Continuation (12 o |
| 32 | 230.2 | 11.0 | 1368 | 2 | AR319163 | AR319163 Sequence |
| 33 | 226.2 | 10.8 | 110000 | 14 | CR543861_10 | Continuation (11 o |
| 34 | 216.8 | 10.3 | 110000 | 14 | CP000473_005 | Continuation (6 of |
| 35 | 198.4 | 9.4 | 110000 | 14 | CP000474_03 | Continuation (4 of |
| c 36 | 194.2 | 9.2 | 110000 | 14 | CP000325_38 | Continuation (39 o |
| 37 | 192.6 | 9.2 | 110000 | 14 | AM711867_00 | AM711867 Clavibact |
| 38 | 185.6 | 8.8 | 110000 | 14 | CP000449_31 | Continuation (32 o |
| 39 | 182.4 | 8.7 | 110000 | 14 | CP000353_01 | Continuation (2 of |
| 40 | 180.2 | 8.6 | 110000 | 14 | CP000117_11 | Continuation (12 o |
| c 41 | 167.8 | 8.0 | 110000 | 14 | CP000473_067 | Continuation (68 o |
| c 42 | 167.4 | 8.0 | 110000 | 14 | BA000019_35 | Continuation (36 o |
| 43 | 164.2 | 7.8 | 110000 | 14 | AE014292_03 | Continuation (4 of |
| c 44 | 163.4 | 7.8 | 110000 | 14 | BX571966_08 | Continuation (9 of |
| c 45 | 163.4 | 7.8 | 110000 | 14 | CP000011_08 | Continuation (9 of |

ALIGNMENTS

RESULT 1
CQ817719
LOCUS CQ817719 2100 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 1 from Patent EP1424397.
ACCESSION CQ817719
VERSION CQ817719.1 GI:48426722
KEYWORDS .
SOURCE Brevibacterium flavum

| | | | |
|----|-------|---|-------|
| Qy | 61 | TCGGCCCGGCTGCACCGTCACGCTTCGAGAAATAGAAATAGCGCTTGTGCAGGCCACCC- | 119 |
| Db | 28439 | TCGGCCCGGCTGCACCGTCACGCTTCGAGAAATAGAAATAGCGCTTGTGCAGGCCACCCCT | 28380 |
| Qy | 120 | -----CACTCTCAACGGCAGCGCCACGCGCTGGCATCAGCCAGGATTTATTAGGA | 171 |
| Db | 28379 | CAACGGCAGCGCCACGAGCGCTGTGCCAGCGCTGGCATCAGCCAGGATTTATTAGGA | 28320 |
| Qy | 172 | CCGGCGATATAGGTAATGGAGTGGCACCCTTGATCCACCAATGCACCACGCTTCGCC | 231 |
| Db | 28319 | CCGGCGATATAGGTAATGGAGCGCACCCCTGATCCACCAATGCACCACGCTTCGCC | 28260 |
| Qy | 232 | GTACCGTCGTAGTTATCCACCATCACGCTGGGAATACCTTGCACCTTCACGGCTCATTAA | 291 |
| Db | 28259 | GCACCGTCGTAGTTATCCACCATCACGCTGGGAATACCTTGCACCTTCACGGCTCATTAA | 28200 |
| Qy | 292 | ACAGTGGGAATTTCCCGCGCAGCTTTGTGGATCTCACCAGAAATCCATCCTTGAAGCAGCG | 351 |
| Db | 28199 | ACAGTGGGAATTTCCCGCGCAGCTTTGTGGATCTCACCAGAAATCCATCCTTGAAGCAGCG | 28140 |
| Qy | 352 | AGCAATAAGCCATCGGCGTGGGGACGATCTTGTCCAGCACCTCCCTGGACTTAATCGCC | 411 |
| Db | 28139 | AGCAATAAGCCATCGGCGTGGGGACGATCTTGTCCAGCACCTCCCTGGACTTAATCGCC | 28080 |
| Qy | 412 | GACTCCCGGGCGTCGACAAGCGCAACCGTATAGCCCTGAGTGCTTGCGGCATGCTGCCG | 471 |
| Db | 28079 | GACTCCCGGGCGTCGACAAGCGCAACCGTATAGCCCTGAGTGCTTGCGGCATGCTGCCG | 28020 |
| Qy | 472 | CCCTGGAAAAATTTCCAAGAAGAGGGATTTCGATGCATCGTGCGCAACCATAGCGATGATA | 531 |
| Db | 28019 | CCCCGAAAAATTTCCAAGAAGAGGGATTTCGACGCATCGCGGCAACCATAGCGATGAGG | 27960 |
| Qy | 532 | CCGGTGTTTTGGCGCTGAAAAGCCTGAGTTTCCACACGCGTTCGGGATTTTCTCCGCAGT | 591 |
| Db | 27959 | CCGGTGTTTTGGCGCTGAAAAGCCTGAGTTTCCACACGCGTTCGGGATTTTCTCCGCAGT | 27900 |
| Qy | 592 | GGAAAACTCACTCGCCAGGCTGCGAAAAACGCCGCGACAGTGGAAAGGGAGACGCC | 651 |
| Db | 27899 | GGAAAACTCACTCGCCAGGCTGCGAAAAACGCCGCGACAGTGGAAAGGGAGACGCC | 27840 |
| Qy | 652 | AGCGACTTTTGGCAGCATATAAATGGTGGCTTTTGAGTCGCTGIG-GCCCCAGAAATCTGT | 710 |
| Db | 27839 | AGCGACTTTTGGCAGCATATAAATGGTGGCTTTTGAGTCGCTGAGCCCCAGAAATCTGT | 27780 |
| Qy | 711 | CATGCACAAGAGTATATAGCGCAAAAGAAATCACTAGTCTTGATTCTATGTTGACGATGC | 770 |
| Db | 27779 | CATGCACAAGAGTATATAGCGCAAAAGAAATCACTAGTCTTGATTCTATGTTGACGATGC | 27720 |
| Qy | 771 | CGATACCCGAGTACCTGCACGAAATTTTAGATGATGTCGCGGACACCACTCCGGCGAGT | 830 |
| Db | 27719 | CGATACCCGAGTACCTGCACGAAATTTTAGATGATGTCGCGGACACCACTCCGGCGAGT | 27660 |
| Qy | 831 | TGGCCGATTACATCCCGGAATAAATATCGCCACCCAAACCCGCTGGCAGTAGCCCTGT | 890 |
| Db | 27659 | TGGCCGATTACATCCCGGAATAAATATCGCGGACCCAAACCCGCTGGCAGTAGCCCTGT | 27600 |

Qy 1 CACAAAATCCGGGAATCCACCGAAATCGTCTTCATCTTTGGCTTGATCAAAATGCCTCAT 60
|||||
Db 28499 CACAAAATCCGGGAATCCACCGAAATCGTCTTCATCTTTGGCTTGATCAAAATGCCTCAT 28440

Qy 891 GCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCATGCAAA 950
 Db 27599 GCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCATGCAAA 27540

Qy 951 GTATTTCCAAGCCCTTTGCCTACGCACTCGCACTCCAAGAATGCGGCTTTGATGAGGTCT 1010
 Db 27539 GTATTTCCAAGCCATTTGCCTACGCACTCGCACTCCAAGAATGCGGCTTTGATGAGGTCT 27480

Qy 1011 CTGCATCCGTGGCTTGGAACTCCGGTGAGGCTTCAACGAACCTTCCCTCGACGCG 1070
 Db 27479 CTGCATCCGTGGCTTGGAGCCCTCCGGTGAGGCTTCAACGAACCTTCCCTCGACGCG 27420

Qy 1071 AAAACCGCCCCATGAACCCCATGATCAACGCCGCGCGATGCCATCAACAGCTGATCA 1130
 Db 27419 AAAACCGCCCCATGAACCCCATGATCAACGCCGCGCGATGCCATCAACAGCTGATCA 27360

Qy 1131 ACGGCTCCGACTCCACCTGGGAAGACCGAGTGGAAAAATCCGACACTACTTCTCTGAAC 1190
 Db 27359 ACGGCTCCGATTCCACCTGGGAAGACCGCGTGGAAAAATCCGACACTACTTCTCTGAAC 27300

Qy 1191 TTGCTGGACGGAACCTACCATCGACGCGTCTTGCCTGAATCCGAATCGCCGCGCG 1250
 Db 27299 TTGCTGGACGGAACCTACCATCGACGCGTCTTGCCTGAATCCGAATCGCCGCGCG 27240

Qy 1251 ACCGCAACCTCTCCATCGCCACATGCTGCGCAACTATGCGGTATCGAAGACGAAGCCC 1310
 Db 27239 ACCGCAACCTCTCCATCGCCACATGCTGCGCAATACGCGGTATCGAAGACGAAGCCC 27180

Qy 1311 ACGACGCCGCTCTCAGTACACGCTGCAATGTGCCATCAAGTAACACGCGGACCTCG 1370
 Db 27179 ACGACGCCGCTCTCAGTACACGCTGCAATGTGCCATCAAGTAACACGCGGACCTCG 27120

Qy 1371 CAGTCATGACCGCCACGCTCGCCGCGGCGGACGACCCCAATTACCGGCAAGAAGCTTC 1430
 Db 27119 CAGTCATGACCGCCACGCTCGCCGCGGCGGACGACCCCAATTACCGGCAAGAAGCTTC 27060

Qy 1431 TCGACGCCGCGTCTGCGGCTCACCCTCTCCGTATGGCTTCAGCAGGCATGTACGACG 1490
 Db 27059 TCGACGCCGCGTCTGCGGCTCACCCTCTCCGTATGGCTTCAGCAGGCATGTACGACG 27000

Qy 1491 AGGCAGGCGAGTGGCTCTCCACCTAGGCATCCCCGCGAAATCAGGAGTCGCCGCGGAC 1550
 Db 26999 AGGCAGGCGAGTGGCTCTCCACCTAGGCATCCCCGCGAAATCAGGAGTCGCCGCGGAC 26940

Qy 1551 TCATCGGCATTCTGCCAGGTGAGTGGGATCGGCACATTTTCCCGACGCTGAACCCCA 1610
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Qy 1611 AAGGCAACAGCGTGCAGGCGTAAAAATATTCAACAGCTTTCCGACGACATGGGCTCC 1670
 Db 26879 AAGGCAACAGCGTGCAGGCGTAAAAATATTCAACAGCTTTCCGACGACATGGGCTCC 26820

Qy 1671 ACCTTATGTCCACCGAGCAGGTATCCGGCCACGAGTACGATCCATTACGCGGACGCG 1730
 Db 26819 ACCTCATGTCCACCGAGCAGGTATCCGGCCACGAGTACGATCCATTACGCGGACGCG 26760

Qy 1731 ACACCACCTTCATCCAAATGCAGGGCGCCATGAACCTTCTCAGCCAGCGAAAGCTTCTCTCC 1790

Db 26759 ACACCACCTTCATCCAAATGCAGGGCGCCATGAACCTTCTCCGCGACGAAAGCTTCTCTCC 26700

Qy 1791 ACGCCATCGTGGAAACAACCTTTGAAGGCACCGAAGTTGTTCTTGATCTCACCAGGTAC 1850
 Db 26699 ACGCCATCGTGGAAACAACCTTTGAAGGCACCGAAGTTGTTCTTGATCTCACCAGGTAC 26640

Qy 1851 TTAGCTTCCACCCCGTAGCCATCCGCATGATCAAGAAGGCGCTCAAACGCATCCGCGACG 1910
 Db 26639 TTAGCTTCCACCCCGTAGCCATCCGCATGATCAAGAAGGCGCTCAAACGCATCCGCGACG 26580

Qy 1911 CAGGCTTTGAGGTGTTCTCTCGACCCAGATGACGTACTGCCGATTTCATGTTTTCCG 1970
 Db 26579 CAGGCTTTGAGGTGTTCTCTCGACCCAGATGACGTACTGCCGATTTCATGTTTTCCG 26520

Qy 1971 ACGGCACCATCTGCAAGAAGCAGTGTGACCGTAGCTTTATGGTCTGAACAATTCGAAG 2030
 Db 26519 ACGGCACCATCTGCAAGAAGCAGTGTGACCGTAGCTTTATGGGCTGAACAATTCGAAG 26460

Qy 2031 GAGATTAATCGGTGAAAAAGAAGCTTATGTTGCCCTTTGATTGTTGCAGCTTTGGGATTA 2090
 Db 26459 GAGAATTATCCGTGAAAAAGAAGCTTATGTTGCCCTTTGATTGTTGCAGCTTTGGGATTA 26400

Qy 2091 GTGCTGCAG 2100
 Db 26399 GTGCTGCAG 26390

RESULT 4

BX927155/c
 LOCUS BX927155 349136 bp DNA linear BCT 14-NOV-2006
 DEFINITION Corynebacterium glutamicum ATCC 13032, IS fingerprint type 4-5, complete genome; segment 8/10.
 ACCESSION BX927155 BX927147
 VERSION BX927155.1 GI:41326514
 KEYWORDS complete genome.
 SOURCE Corynebacterium glutamicum ATCC 13032
 ORGANISM Corynebacterium glutamicum ATCC 13032
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 REFERENCE 1 (bases 1 to 349136)
 AUTHORS Kalinowski,J., Bathe,B., Bartels,D., Bischoff,N., Bott,M., Burkovski,A., Dusch,N., Eggeling,L., Eikmanns,B.J., Gaigalat,L., Goesmann,A., Hartmann,M., Huthmacher,K., Kramer,R., Linke,B., McHardy,A.C., Meyer,F., Mockel,B., Pfefferle,W., Puhler,A., Rey,D.A., Ruckert,C., Rupp,O., Sahn,H., Wendisch,V.F., Wiegrabe,I. and Tauch,A.
 TITLE The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins
 JOURNAL J. Biotechnol. 104 (1-3), 5-25 (2003)
 PUBMED 12948626
 REFERENCE 2 (bases 1 to 349136)
 AUTHORS Kalinowski,J.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2004) Joern Kalinowski, Institut fuer Genomforschung, Universitaet Bielefeld; Universitaetsstrasse 25,